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RAW SEQUENCE LISTING PATENT APPLICATION US/08/836,455

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DATE: 06/23/98 TIME: 13:34:14

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This Raw Listing contains the General Information Section and up to the first 5 pages.

1		SEQUENCE LISTING
2	(1) G	eneral Information:
4 5 6 7 8	(i)	APPLICANT: Chatterjee, Malaya Foon, Kenneth A. Chatterjee, Sunil K.
9 10	(ii)	TITLE OF INVENTION: MURINE MONOCLONAL ANTI-IDIOTYPE ANTIBODY 11D10 AND METHODS OF USE THEREOF
11 12 13	(iii)	NUMBER OF SEQUENCES: 59
14 15 16 17 18 19 20 21	(iv)	CORRESPONDENCE ADDRESS: (A) ADDRESSEE: MORRISON & FOERSTER (B) STREET: 755 PAGE MTEL ROAD (C) CITY: PALO ALTO (D) STATE: CA (E) COUNTRY: USA (F) ZIP: 94304-1018
22 23 24 25 26 27	· (v)	COMPUTER READABLE FORM: (A) MEDIUM TYPE: Floppy disk (B) COMPUTER: IBM PC compatible (C) OPERATING SYSTEM: PC-DOS/MS-DOS (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
28 29 30 31 32	(vi)	CURRENT APPLICATION DATA: (A) APPLICATION NUMBER: US 08/836,455 (B) FILING DATE: 09-MAY-1997 (C) CLASSIFICATION:
33 34 35 36 37	(viii)	ATTORNEY/AGENT INFORMATION: (A) NAME: Polizzi, Catherine M. (B) REGISTRATION NUMBER: 40,130 (C) REFERENCE/DOCKET NUMBER: 30414-20003.22
38 39 40 41 42	(ix)	TELECOMMUNICATION INFORMATION: (A) TELEPHONE: (650) 813-5600 (B) TELEFAX: (650) 494-0792 (C) TELEX: 706141
43 44	(2) INFO	RMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

RAW SEQUENCE LISTING PATENT APPLICATION US/08/836,455

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52		(11)) MOI	LECUI	LE T	PE:	DNA	(gei	nomi	c)							
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62																	
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	64 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1: 65																
	1 mg	GGG	000	aam	aam	a.a	3 000	amm	000	mma	mma	mma	ama	mma	mmm	COA	48
66																	40
67		Gly	АТА	PIO	ATA		тте	Leu	GTĀ	Pne	-10	Leu	Leu	rea	FIIE	-5	
68	-20					-15					-10					-3	
69	aam	ACC	202	mam	a 2 a	» ma	as a	3 mg	3.00	ana	mam	CCA	maa	maa	mm a	mam	96
70		Thr															30
71 72	GIY	THE	Arg	Cys	ASP	TTE	GIN	Met	5	GTII	Ser	PIU	Ser	10	ьеu	Ser	
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73 74	aaa	TCT	ama	CCA	CAA	A CI A	ama	አረሞ	CTC	አረጥ	ጥረጥ	caa	GCA	እርጥ	CAG	GAC	144
75		Ser															
76	Ата	Ser	15	СТУ	GIII	Arg	Val	20	пеп	1111	Cys	ALG	25	561	0111	ADP	
77			13					20					2,5				
78	Δ ТТ	GGT	ΔΨΨ	ΔAC	тπъ	САТ	TGG	СФФ	CAG	CAG	GAA	CCA	GAT	GGA	ACT	АТТ	192
79		Gly															
80		30					35					40		1			
81		•					•-										
82	AAA	CGC	CTG	ATC	TAC	GCC	ACA	TCC	AGT	TTA	GGT	TCT	GGT	GTC	CCC	AAA	240
83		Arg															
84	45					50					55		-			60	
85																	
86	AGG	TTC	AGT	GGC	AGT	AGG	TCT	GGG	TCA	GAT	TAT	TCT	CTC	ACC	ATC	AGC	288
87	Arg	Phe	Ser	Gly	Ser	Arg	Ser	Gly	Ser	Asp	Tyr	Ser	Leu	Thr	Ile	Ser	
88	_				65	_				70					75		
89																	
90		CTT															336
91	Ser	Leu	Glu	Ser	Glu	Asp	Phe	Val	Ala	Tyr	Tyr	Cys	Leu	Gln	Tyr	Ala	
92				80					85					90			
93																	
94	AGT	TCT	CCG	TAC	ACG	TTC	GGA	GGG	GGG	ACC	AAG	CTG	GAA	ATA	AAA	CGG	384
95	Ser	Ser	Pro	Tyr	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Arg	
96			95					100					105				
97																	_
98		GAT															432
99	Ala	Asp	Ala	Ala	Pro	Thr	Val	Ser	Ile	Phe	Pro	Pro	Ser	Ser	Lys	Leu	

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100		110					115					120						
101																		
102	GGG																	435
103	Gly																	
104	125																	
105																		
106																		
107	(2)	INFO	ORMA'	TION	FOR	SEO	ID I	NO:2	:									
108	\ - <i>\</i>					-												
100			(4)	25011	PNOP	CHAI	олет	ERIS	TTCC	•						•		
		,	(1)								_							
110		(A) LENGTH: 145 amino acids (B) TYPE: amino acid																
111		, ,																
112		(D) TOPOLOGY: linear																
113																		
114		(:	ii) l	MOLE	CULE	TYP	E: p:	rote:	in									
115		•	•				-		-									
116		(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:																
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117				_				_		-1 -		•	•	-	D1	D		
118		СТĀ	Ala	Pro	Ala			Leu	GTĀ	Phe		Leu	ren	Leu	Pne			
119	-20					-15					-10					-5		
120																		
121	Glv	Thr	Arq	Cys	Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser		
122	2		3	-	ī				5					10				
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124	АТа	ser		GTÅ	GIN	Arg	val		Leu	Thr	Cys	Arg		ser	GIII	ASP		
125			15					20					25					
126																		
127	Ile	Gly	Ile	Asn	Leu	His	Trp	Leu	Gln	Gln	Glu	Pro	Asp	Gly	Thr	Ile		
128		30					35					40						
129																		
130	Tve	λrα	T. 011	Tla	Туг	ala	Thr	Ser	Ser	Leu	Glv	Ser	Glv	Val	Pro	I.vs		
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131	45					50					33					00		
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133	Arg	Phe	Ser	Gly	Ser	Arg	Ser	Gly	Ser	Asp	Tyr	Ser	Leu	Thr		ser		
134					65					70					75			
135																		
136	Ser	Leu	Glu	Ser	Glu	Asp	Phe	Val	Ala	Tyr	Tyr	Cys	Leu	Gln	Tyr	Ala		
137				80					85	-	•			90	-			
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139	Ser	ser		Tyr	Thr	Pne	GTÅ	_	GTA	Thr	Lys	Leu		тте	гуѕ	Arg		
140			95					100					105					
141																		
142	Ala	Asp	Ala	Ala	Pro	Thr	Val	Ser	Ile	Phe	Pro	Pro	Ser	Ser	Lys	Ļeu		
143		110					115					120				•		
144																		
145	Gly																	
146	125																	
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148	(2)	INF	ORMA'	TION	FOR	SEQ	ID I	10:3	:									
149																		
150		(i) SE	QUEN	CE CI	HARA	CTER	ISTI	CS:									
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153			(C) S'	[RAN]	DEDN	ESS:	sin	gle								
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156		(ii) MOI	LECU	LE T	YPE:	DNA	(ge	nomi	C)							
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159		(ix) FE	ATUR	€:												
160			()	A) N	AME/I	KEY:	CDS										
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170								Leu	-								40
171 172	-19	GIU	cys	Set	-15	vaı	Pne	Leu	Pne	-10	Leu	Ser	116	TIII	-5	СТУ	
173	-19				-13					-10					-3		
174	GTC	CAC	TCC	CAG	COT	ጥልጥ	СТА	CAG	CAG	ጥርጥ	aaa	ССТ	GAG	СТС	стс	ΔGG	96
175								Gln									,,
176	, ,		501	1		- 1 -		5		501	1		10			9	
177				_				_									
178	TCT	GGG	GCC	TCA	GTG	AAG	ATG	TCC	TGC	AAG	GCT	TCT	GGC	TAC	ACA	TTG	144
179								Ser									
180		15				•	20		•	-		25	-	-			
181																	
182	ACC	AGT	TAC	AAT	ATG	CAC	TGG	GTA	AAG	CAG	ACA	CCT	GGA	CAG	GGC	CTG	192
183	Thr	Ser	Tyr	Asn	Met	His	Trp	Val	Lys	Gln	Thr	Pro	Gly	Gln	Gly	Leu	
184	30					35					40					45	
185																	
186								CCT									240
187	Glu	Trp	Ile	Gly		Ile	Phe	Pro	Gly		Gly	Asp	Thr	Tyr	_	Asn	
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190								TCA									288
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195								Ser									330
196		AIU	80	1400	04	110	D C1	85	204	••••	5 01		90	501			
197													- 0				
198	ТАТ	TTC	TGT	GCA	AGA	GGG	AAC	TGG	GAG	GGT	GCT	CTG	GAC	TAC	TGG	GGT	384
199								Trp									
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201																	
202	CAA	GGA	ACC	TCA	GTC	ACC	GTC	TCC	TCA	GCC	AAA	ACG	ACA	CCC	CCA	CCC	432
203								Ser									
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206	GTC	TAT	CCA	CTG	GTC	CCT	GGA	AGC	TTG	GG							461
207							Gly										
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222		GIU	Cys	Set	_	Val	Pne	Leu	Pne		Leu	Ser	TTE	1111		GIY	
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225	Val	His	Ser	Gln	Ala	Tyr	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Arg	
226				1				5					10				
227																	
228	Sor	<i>G</i>] v	Δla	Ser	Val	T.VS	Met	Ser	CVS	I.vs	Δla	Ser	Glv	Tur	Thr	Leu	
229	Ser	-	AIG	JCI	vul	2,5	20	001	0,5	2,5	n_u	25	- 1	- 1 -		204	
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233																	
234	Glu	Trp	Ile	Glv	Asn	Ile	Phe	Pro	Glv	Asn	Glv	Asp	Thr	Tvr	Tvr	Asn	
235					50					55	- 4	-		-	60		
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240	Thr	Ala	Tyr	Met	Gln	Ile	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	
241			80					85					90				
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243	Пать	Dhe	Cve	λla	Ara	G] v	Asn	Trn	Glu	Glv	Δla	T.e.11	Asn	Tur	Trn	Gl v	
244	- 7 -	95	Cys	AIU	nr 9	OT,	100		014	1	****	105	шь	-] -		- 1	
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245	_	_	_								_			_	_	_	
246		Gly	Thr	Ser	Val		Val	Ser	Ser	A⊥a	_	Thr	Thr	Pro	Pro		
247	110					115					120					125	
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249	Val	Tvr	Pro	Leu	Val	Pro	Gly	Ser	Leu								
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